

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 03:26:18 ; Search time 154 Seconds  
(without alignments)  
7560.305 Million cell updates/sec

Title: US-09-445-223-2  
Perfect score: 2098  
Sequence: 1 ggcattatggatgggg.....aaaaaaaaaaaaaaaaaaaaa 2098

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
  - 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
  - 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
  - 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
  - 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
  - 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	32	1.5	36	4	US-09-462-569B-4	Sequence 4, Appli
C 2	32	1.5	37	1	US-08-113-646A-44	Sequence 44, Appl
C 3	32	1.5	38	4	US-09-720-201A-19	Sequence 19, Appl
C 4	32	1.5	40	2	US-08-771-624B-1	Sequence 1, Appli
C 5	32	1.5	40	2	US-08-440-209-4	Sequence 4, Appli
C 6	32	1.5	40	3	US-08-439-996-4	Sequence 4, Appli
C 7	32	1.5	40	4	US-09-732-067-7	Sequence 7, Appli
C 8	32	1.5	50	1	US-08-420-443-1	Sequence 1, Appli
C 9	32	1.5	50	4	US-09-621-976-14612	Sequence 14612, A
C 10	32	1.5	50	4	US-09-621-976-14715	Sequence 14715, A
C 11	31	1.5	41	4	US-08-197-814-9	Sequence 9, Appli
C 12	31	1.5	41	4	US-09-920-581-9	Sequence 9, Appli
C 13	31	1.5	43	4	US-09-165-239A-5	Sequence 5, Appli
C 14	31	1.5	44	1	US-08-664-596B-9	Sequence 9, Appli
C 15	31	1.5	45	4	US-09-894-916-3	Sequence 3, Appli
C 16	30	1.4	30	1	US-08-433-505-9	Sequence 9, Appli
C 17	30	1.4	30	3	US-08-870-730-9	Sequence 9, Appli
C 18	30	1.4	30	4	US-09-083-123-3	Sequence 3, Appli
C 19	30	1.4	30	4	US-09-083-123-7	Sequence 7, Appli
C 20	30	1.4	30	4	US-08-882-649A-10	Sequence 10, Appl
C 21	30	1.4	31	4	US-09-268-505B-13	Sequence 13, Appl
C 22	30	1.4	33	3	US-09-061-026-26	Sequence 26, Appl
C 23	30	1.4	33	3	US-09-466-138-26	Sequence 26, Appl
C 24	30	1.4	42	1	US-07-875-167-2	Sequence 2, Appli
C 25	30	1.4	42	1	US-08-287-164-2	Sequence 2, Appli
C 26	30	1.4	47	2	US-08-778-494B-114	Sequence 114, App
C 27	30	1.4	48	4	US-09-738-274-35	Sequence 35, Appl

C 28	30	1.4	50	1	US-08-233-609-5	Sequence 5, Appli
C 29	30	1.4	50	1	US-08-381-572-20	Sequence 20, Appl
C 30	30	1.4	50	1	US-08-444-083-5	Sequence 5, Appli
C 31	30	1.4	50	1	US-08-286-304-5	Sequence 5, Appli
C 32	30	1.4	50	1	US-08-442-745-5	Sequence 5, Appli
C 33	30	1.4	50	1	US-08-443-129-5	Sequence 5, Appli
C 34	30	1.4	50	1	US-08-443-952-5	Sequence 5, Appli
C 35	30	1.4	50	1	US-08-443-130-5	Sequence 5, Appli
C 36	30	1.4	50	1	US-08-592-820-20	Sequence 20, Appl
C 37	30	1.4	50	3	US-08-898-911-5	Sequence 5, Appli
C 38	30	1.4	50	5	PCT-US95-04467-5	Sequence 5, Appli
C 39	29	1.4	42	3	US-09-244-794A-11	Sequence 11, Appl
C 40	29	1.4	42	3	US-09-244-794A-12	Sequence 12, Appl
C 41	29	1.4	42	3	US-09-244-794A-13	Sequence 13, Appl
C 42	29	1.4	42	3	US-09-247-190-11	Sequence 11, Appl
C 43	29	1.4	42	3	US-09-247-190-12	Sequence 12, Appl
C 44	29	1.4	42	3	US-09-247-190-13	Sequence 13, Appl
C 45	29	1.4	42	4	US-09-238-710-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
 US-09-462-569B-4/C  
 ; Sequence 4, Application US/09462569B  
 ; Patent No. 6392124  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PONZ ASCASO, Fernando  
 ; APPLICANT: TORRES PASCUAL, Vicente  
 ; APPLICANT: SANCHEZ SANCHEZ, Florentina  
 ; APPLICANT: MARTINEZ HERRERA, David  
 ; TITLE OF INVENTION: INFECTIOUS VECTORS AND CLONES OF PLANTS DERIVED FROM  
 ; TITLE OF INVENTION: THE TURNIP MOSAIC VIRUS (TUMV)  
 ; FILE REFERENCE: P/613-110  
 ; CURRENT APPLICATION NUMBER: US/09/462,569B  
 ; CURRENT FILING DATE: 2000-04-03  
 ; PRIOR APPLICATION NUMBER: PCT/ES98/00200  
 ; PRIOR FILING DATE: 1998-07-09  
 ; PRIOR APPLICATION NUMBER: ES P 9701522  
 ; PRIOR FILING DATE: 1997-07-09  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 36  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: construct  
 ; OTHER INFORMATION: construct  
 US-09-462-569B-4

Query Match Best Local Similarity 1.5%; Score 32; DB 4; Length 36;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 2  
 US-08-113-646A-44  
 ; Sequence 44, Application US/08113646A  
 ; Patent No. 5578468  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PICKUP, David J.  
 ; APPLICANT: PATEL, DhavalKumar  
 ; APPLICANT: ANTCAK, James B.  
 ; TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: NIXON & VANDERHYE P. C.

STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/113,646A  
 FILING DATE: 31-AUG-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/084,406  
 FILING DATE: 10-AUG-1987  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WILSON, MARY J.  
 REGISTRATION NUMBER: 32,955  
 REFERENCE/DOCKET NUMBER: 1579-20  
 TELEPHONE: (703) 816-4000  
 TELEFAX: (703) 816-4100  
 TELEX: 200797 NIXN UR 44:  
 INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 37 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: RNA (genomic)  
 US-08-113-646A-44

Query Match 1.5%; Score 32; DB 1; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 3  
 US-09-720-201A-19/c  
 ; Sequence 19, Application US/09720201A  
 ; Patent No. 6524853  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KOHARA, MICHINORI  
 ; APPLICANT: KOHARA, KYOKO  
 ; APPLICANT: TAIRA, KAZUNARI  
 ; APPLICANT: MATSUZAKI, JUNICHI  
 ; APPLICANT: OHMORI, HIROSHI  
 ; TITLE OF INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH GENE AND  
 ; TITLE OF INVENTION: ITS USE  
 ; FILE REFERENCE: 04853.0051-00000  
 ; CURRENT APPLICATION NUMBER: US/09/720,201A  
 ; CURRENT FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: JP 98/177,820  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: PCT/JP99/03381  
 ; PRIOR FILING DATE: 1999-06-24  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 19  
 ; LENGTH: 38  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer  
 US-09-720-201A-19

Query Match 1.5%; Score 32; DB 4; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 4  
 US-08-771-624B-1/c  
 ; Sequence 1, Application US/08771624B  
 ; Patent No. 5914230  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Yen Ping  
 ; APPLICANT: Patel, Rajesh D.  
 ; APPLICANT: Kurn, Nurith  
 ; APPLICANT: Lin, Claire  
 ; APPLICANT: Rose, Samuel J.  
 ; APPLICANT: Ullman, Edwin F.  
 ; TITLE OF INVENTION: Homogeneous Amplification and Detection  
 ; TITLE OF INVENTION: Of Nucleic Acids  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Behring Diagnostics GmbH, c/o Dade Behring Inc.  
 ; STREET: 1717 Deerfield Road  
 ; CITY: Deerfield  
 ; STATE: Illinois  
 ; COUNTRY: US  
 ; ZIP: 60015-0778  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/771,624B  
 ; FILING DATE: 20-DEC-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/009,090  
 ; FILING DATE: 22-DEC-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ruzsala, Lois K.  
 ; REGISTRATION NUMBER: 39,074  
 ; REFERENCE/DOCKET NUMBER: 1030  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (847) 267-5364  
 ; TELEFAX: (847) 267-6024  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 40 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: C-terminal  
 ; US-08-771-624B-1

Query Match 1.5%; Score 32; DB 2; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 5  
 US-08-440-209-4/c  
 ; Sequence 4, Application US/08440209

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; Patent No. 5922857
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,209
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,895
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/128,583
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-440-209-4

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,996
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,895A
; FILING DATE:
; APPLICATION NUMBER: US 08/128,583
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-439-996-4

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Query Match 1.5%; Score 32; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

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Query Match 1.5%; Score 32; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

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RESULT 7
US-09-732-067-7
; Sequence 7, Application US/09732067
; Patent No. 6457426
; GENERAL INFORMATION:
; APPLICANT: Ullman, Edwin
; APPLICANT: Singh, Rajendra
; APPLICANT: Dekecz, Steve
; APPLICANT: Davalian, Dariush
; TITLE OF INVENTION: Amplified Luminescent Homogeneous
; TITLE OF INVENTION: Immunoassay
; FILE REFERENCE: BEH-7385
; CURRENT APPLICATION NUMBER: US/09/732,067
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hybridization oligo
; US-09-732-067-7

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RESULT 6
US-08-439-996-4/C
; Sequence 4, Application US/08439996
; Patent No. 6057093
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:

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Query Match 1.5%; Score 32; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

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Query Match 1.5%; Score 32; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

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RESULT 8  
 US-08-420-443-1  
 ; Sequence 1, Application US/08420443  
 ; Patent No. 5607834  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Bruce Bagwell  
 ; TITLE OF INVENTION: NUCLEIC ACID PROBES  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX  
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/420,443  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/990,298  
 ; FILING DATE: 19921210  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Y. Rocky Tsao  
 ; REGISTRATION NUMBER: 34,053  
 ; REFERENCE/DOCKET NUMBER: 05663/002001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 542-5070  
 ; TELEFAX: (617) 542-8906  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 50  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-420-443-1

Query Match 1.5%; Score 32; DB 1; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 9  
 US-09-621-976-14612  
 ; Sequence 14612, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 14612  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-621-976-14612

Query Match 1.5%; Score 32; DB 4; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 10  
 US-09-621-976-14715  
 ; Sequence 14715, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 14715  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-621-976-14715

Query Match 1.5%; Score 32; DB 4; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 11  
 US-09-197-814-9/c  
 ; Sequence 9, Application US/09197814A  
 ; Patent No. 6316220  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Christensen, Tove  
 ; TITLE OF INVENTION: A Transcription Factor  
 ; FILE REFERENCE: 4484.204-US  
 ; CURRENT APPLICATION NUMBER: US/09/197,814A  
 ; CURRENT FILING DATE: 1998-11-23  
 ; EARLIER APPLICATION NUMBER: 0740/96  
 ; EARLIER FILING DATE: 1996-07-05  
 ; EARLIER APPLICATION NUMBER: PCT/DK97/00305  
 ; EARLIER FILING DATE: 1997-07-07  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 41  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-09-197-814-9

Query Match 1.5%; Score 31; DB 4; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 0.00055;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2097  
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11

RESULT 12  
 US-09-920-581-9/c

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; Sequence 9, Application US/09920581
; Patent No. 6555657
; GENERAL INFORMATION:
; APPLICANT: Christensen, Tove
; TITLE OF INVENTION: A Transcription Factor
; FILE REFERENCE: 4484.204-US
; CURRENT APPLICATION NUMBER: US/09/920,581
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/197,814
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: PCT/DK97/00305
; PRIOR FILING DATE: 1997-07-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-920-581-9

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Query Match 1.5%; Score 31; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2097
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11

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RESULT 13
US-09-165-239A-5/c
; Sequence 5, Application US/09165239A
; Patent No. 6344554
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, ALEXANDER
; APPLICANT: BRAUN, BURKHARD R
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES FROM CANDIDA
; TITLE OF INVENTION: ALBICANS ENCODING POLYPEPTIDES ASSOCIATED WITH FILAMENTOUS
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: 220022000700
; CURRENT APPLICATION NUMBER: US/09/165,239A
; CURRENT FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/068,065
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-165-239A-5

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Query Match 1.5%; Score 31; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2097
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 13

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RESULT 14
US-08-664-596B-9
; Sequence 9, Application US/08664596B
; Patent No. 5807703
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Lavallie, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Merberg, David

```

```

; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; APPLICANT: Spaulding, Vikki
; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,596B
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-664-596B-9

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Query Match 1.5%; Score 31; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2096
Db 14 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44

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RESULT 15
US-09-894-916-3/c
; Sequence 3, Application US/09894916
; Patent No. 6642361
; GENERAL INFORMATION:
; APPLICANT: Hunter, Fiona F.
; APPLICANT: Bidochka, Michael J.
; TITLE OF INVENTION: Isolated Cocoon Silk Protein From Simulium Vittatum And Nucleic A
; TITLE OF INVENTION: Encoding Such Protein
; FILE REFERENCE: 1468-001A
; CURRENT APPLICATION NUMBER: US/09/894,916
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214992
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Simulium vittatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44)..(45)
; OTHER INFORMATION: n can be any of A, T, G or C
US-09-894-916-3

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Query Match 1.5%; Score 31; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2096
Db 14 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44

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RESULT 15
US-09-894-916-3/c
; Sequence 3, Application US/09894916
; Patent No. 6642361
; GENERAL INFORMATION:
; APPLICANT: Hunter, Fiona F.
; APPLICANT: Bidochka, Michael J.
; TITLE OF INVENTION: Isolated Cocoon Silk Protein From Simulium Vittatum And Nucleic A
; TITLE OF INVENTION: Encoding Such Protein
; FILE REFERENCE: 1468-001A
; CURRENT APPLICATION NUMBER: US/09/894,916
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214992
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Simulium vittatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44)..(45)
; OTHER INFORMATION: n can be any of A, T, G or C
US-09-894-916-3

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Query Match 1.5%; Score 31; DB 4; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.00055;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2097  
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 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 13

Search completed: July 2, 2004, 07:38:41  
 Job time : 158 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 03:36:20 ; Search time 1830 Seconds  
(without alignments)  
5530.704 Million cell updates/sec

Title: US-09-445-223-2  
Perfect score: 2098  
Sequence: 1 ggcattatgatgatggg.....aaaaaaaaaaaaaaaaaaaaa 2098

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3163042 seqs, 2412103800 residues

Word size : 0 1726952

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

- Database :
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  - 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
  - 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
  - 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
  - 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
  - 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
  - 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
  - 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
  - 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
  - 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
  - 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
  - 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
  - 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2.\*
  - 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
  - 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
  - 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
  - 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
  - 18: /cgn2\_6/ptodata/2/pubpna/US50\_NEW\_PUB.seq.\*
  - 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-Result No.	Score	Query Match	Length	DB ID	Description
1	50	2.4	50	16	US-10-131-827-4651
C 2	34	1.6	45	9	US-09-827-289-14
C 3	34	1.6	45	9	US-09-827-289-18
C 4	34	1.6	45	9	US-09-827-289-21
C 5	34	1.6	45	9	US-09-827-289-25
C 6	33	1.6	36	9	US-09-828-034-2
C 7	33	1.6	36	9	US-09-828-034-3
C 8	33	1.6	45	9	US-09-827-289-22
C 9	33	1.6	45	9	US-09-827-289-26
-C 10	32	1.5	32	15	US-10-371-600-2
-C 11	32	1.5	32	15	US-10-371-600-9
C 12	32	1.5	32	15	US-10-371-600-10
C 13	32	1.5	38	10	US-09-764-891-10175
C 14	32	1.5	39	15	US-10-289-921-6

C 15	32	1.5	40	13	US-10-463-549-26
C 16	32	1.5	43	15	US-10-218-567-7
C 17	32	1.5	43	15	US-10-352-253A-37
C 18	32	1.5	47	10	US-09-764-891-10177
C 19	32	1.5	47	15	US-10-289-921-5
C 20	32	1.5	48	17	US-10-082-188-107
C 21	32	1.5	48	17	US-10-668-749A-4
C 22	32	1.5	50	9	US-09-815-343-1012
C 23	32	1.5	50	13	US-10-097-105-1012
C 24	31	1.5	41	9	US-09-920-581-9
C 25	31	1.5	41	15	US-10-371-421-9
C 26	31	1.5	43	10	US-09-932-165-1485
C 27	31	1.5	43	10	US-09-942-052-714
C 28	31	1.5	43	13	US-10-013-312-2995
C 29	31	1.5	43	13	US-10-087-190-30
C 30	31	1.5	43	15	US-10-121-019-13
C 31	31	1.5	43	16	US-10-120-885A-28
C 32	31	1.5	43	16	US-10-121-016-55
C 33	31	1.5	43	16	US-10-114-669-6
C 34	31	1.5	43	16	US-10-114-432-42
C 35	31	1.5	45	10	US-09-894-916-3
C 36	30	1.4	30	13	US-09-880-727-10
C 37	30	1.4	30	13	US-10-314-578-1094
C 38	30	1.4	30	14	US-10-314-578-1095
C 39	30	1.4	30	14	US-10-042-193A-1
C 40	30	1.4	30	14	US-10-042-193A-2
C 41	30	1.4	30	16	US-10-380-584-115
C 42	30	1.4	32	15	US-10-371-600-3
C 43	30	1.4	32	15	US-10-371-600-4
C 44	30	1.4	39	15	US-10-219-195-28
C 45	30	1.4	39	15	US-10-219-195-29

ALIGNMENTS

RESULT 1  
 US-10-131-827-4651  
 ; Sequence 4651, Application US/10131827  
 ; Publication No. US20040009479A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgemuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
 ; FILE REFERENCE: 506612000120  
 ; CURRENT APPLICATION NUMBER: US/10/131,827  
 ; CURRENT FILING DATE: 2002-09-06  
 ; PRIOR APPLICATION NUMBER: US 10/006,290  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/296,764  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 9090  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4651  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-131-827-4651

Query Match 2.4%; Score 50; DB 16; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-14;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1803 TGGGTCTTCAGCCTTACCCGAAATCTTGGTTCCTAGATCACCATCT 1852  
 |||||  
 Db 1 TGGGTCTTCAGCCTTACCCGAAATCTTGGTTCCTAGATCACCATCT 50  
 |||||

RESULT 2  
US-09-827-289-14/c





; SEQ ID NO 2  
 ; LENGTH: 36  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA  
 US-09-828-034-2

Query Match 1.6%; Score 33; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 7  
 US-09-828-034-3  
 ; Sequence 3, Application US/09828034  
 ; Patent No. US20020064771A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhong, Weidong  
 ; APPLICANT: Hong, Zhi  
 ; APPLICANT: Ferrari, Eric  
 ; TITLE OF INVENTION: HCV REPLICASE COMPLEXES  
 ; FILE REFERENCE: IN01165  
 ; CURRENT APPLICATION NUMBER: US/09/828,034  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: U.S. 60/195,852  
 ; PRIOR FILING DATE: 2000-04-06  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 36  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA  
 US-09-828-034-3

Query Match 1.6%; Score 33; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 8  
 US-09-827-289-22/c  
 ; Sequence 22, Application US/09827289  
 ; Patent No. US20020009716A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abarzuza, Patricia  
 ; TITLE OF INVENTION: Process for Allele Discrimination Using Primer  
 ; FILE REFERENCE: Extension  
 ; CURRENT APPLICATION NUMBER: US/09/827,289  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: U.S. 60/194843  
 ; PRIOR FILING DATE: 2000-04-05  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 46  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for  
 ; OTHER INFORMATION: use in allele discrimination  
 US-09-827-289-22

Query Match 1.5%; Score 32; DB 15; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 10  
 US-10-371-600-2/c  
 ; Sequence 2, Application US/10371600  
 ; Publication No. US20030180776A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WU, MING  
 ; APPLICANT: ULLMAN, EDWIN F.  
 ; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION  
 ; FILE REFERENCE: 3817.10-2  
 ; CURRENT APPLICATION NUMBER: US/10/371,600  
 ; CURRENT FILING DATE: 2003-05-19  
 ; PRIOR APPLICATION NUMBER: 60/359,223  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: 60/379,360  
 ; PRIOR FILING DATE: 2002-05-08  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 32  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-371-600-2

Query Match 1.6%; Score 33; DB 9; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 38 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 9  
 US-09-827-289-26/c  
 ; Sequence 26, Application US/09827289  
 ; Patent No. US20020009716A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abarzuza, Patricia  
 ; TITLE OF INVENTION: Process for Allele Discrimination Using Primer  
 ; FILE REFERENCE: Extension  
 ; CURRENT APPLICATION NUMBER: US/09/827,289  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: U.S. 60/194843  
 ; PRIOR FILING DATE: 2000-04-05  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 26  
 ; LENGTH: 46  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for  
 ; OTHER INFORMATION: use in allele discrimination  
 US-09-827-289-26

Query Match 1.6%; Score 33; DB 9; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 38 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 10  
 US-10-371-600-2/c  
 ; Sequence 2, Application US/10371600  
 ; Publication No. US20030180776A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WU, MING  
 ; APPLICANT: ULLMAN, EDWIN F.  
 ; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION  
 ; FILE REFERENCE: 3817.10-2  
 ; CURRENT APPLICATION NUMBER: US/10/371,600  
 ; CURRENT FILING DATE: 2003-05-19  
 ; PRIOR APPLICATION NUMBER: 60/359,223  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: 60/379,360  
 ; PRIOR FILING DATE: 2002-05-08  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 32  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-371-600-2

Query Match 1.5%; Score 32; DB 15; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 8  
 US-09-827-289-22/c  
 ; Sequence 22, Application US/09827289  
 ; Patent No. US20020009716A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abarzuza, Patricia  
 ; TITLE OF INVENTION: Process for Allele Discrimination Using Primer  
 ; FILE REFERENCE: Extension  
 ; CURRENT APPLICATION NUMBER: US/09/827,289  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: U.S. 60/194843  
 ; PRIOR FILING DATE: 2000-04-05  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 46  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for  
 ; OTHER INFORMATION: use in allele discrimination  
 US-09-827-289-22

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11  
 US-10-371-600-9  
 ; Sequence 9, Application US/10371600  
 ; Publication No. US20030180776A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WU, MING  
 ; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION  
 ; FILE REFERENCE: 3817.10-2  
 ; CURRENT APPLICATION NUMBER: US/10/371,600  
 ; PRIOR FILING DATE: 2003-05-19  
 ; PRIOR APPLICATION NUMBER: 60/359,223  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: 60/379,360  
 ; PRIOR FILING DATE: 2002-05-08  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 32  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-371-600-9

Query Match 1.5%; Score 32; DB 15; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 12  
 US-10-371-600-10/c  
 ; Sequence 10, Application US/10371600  
 ; Publication No. US20030180776A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WU, MING  
 ; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION  
 ; FILE REFERENCE: 3817.10-2  
 ; CURRENT APPLICATION NUMBER: US/10/371,600  
 ; PRIOR FILING DATE: 2003-05-19  
 ; PRIOR APPLICATION NUMBER: 60/359,223  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: 60/379,360  
 ; PRIOR FILING DATE: 2002-05-08  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 32  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-371-600-10

Query Match 1.5%; Score 32; DB 15; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 13  
 US-09-764-891-10175  
 ; Sequence 10175, Application US/09764891  
 ; Publication No. US20030077808A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PC006  
 ; CURRENT APPLICATION NUMBER: US/09/764,891  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 10231  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10175  
 ; LENGTH: 38  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-764-891-10175

Query Match 1.5%; Score 32; DB 10; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 14  
 US-10-289-921-6/c  
 ; Sequence 6, Application US/10289921  
 ; Publication No. US20030113337A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MERUELO, Daniel  
 ; APPLICANT: OHNO, Kouichi  
 ; APPLICANT: LEVIN, Brandi A.  
 ; TITLE OF INVENTION: HIGH EFFICIENCY TISSUE SPECIFIC COMPOUND  
 ; DELIVERY SYSTEM USING STREPTAVIDIN-PROTEIN A FUSION PROTEIN  
 ; FILE REFERENCE: 5986/11123-US1  
 ; CURRENT APPLICATION NUMBER: US/10/289,921  
 ; CURRENT FILING DATE: 2003-02-27  
 ; PRIOR APPLICATION NUMBER: US 08/566,421  
 ; PRIOR FILING DATE: 1995-11-30  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 39  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: biotinylated poly(dT) oligonucleotide  
 US-10-289-921-6

Query Match 1.5%; Score 32; DB 15; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 15  
 US-10-463-549-26/c  
 ; Sequence 26, Application US/10463549  
 ; Publication No. US20040053308A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nakamura, Kumi  
 ; TITLE OF INVENTION: Probe Immobilized Substrate and Method for Manufacturing the Same  
 ; TITLE OF INVENTION: Analytical Method  
 ; FILE REFERENCE: 03560.003309

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; CURRENT APPLICATION NUMBER: US/10/463,549
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 2002-190009
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 2002-189836
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 26
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-463-549-26

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Query Match      1.5%; Score 32; DB 13; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

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Search completed: July 2, 2004, 08:09:22
Job time : 1834 secs

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INIS PAGE BILUK (USPIO)

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
 Run on: July 2, 2004, 03:25:48 ; Search time 5407 Seconds  
 (without alignments)  
 11586.990 Million cell updates/sec  
 Title: US-09-445-223-2  
 Perfect score: 2098  
 Sequence: 1 ggcattatggtggtggg.....aaaaaaaaaaaaaaaaaaaaa 2098

Scoring table: OLIGO\_NUC  
 Gapop 60.0 , Gapext 60.0  
 Searched: 27513289 seqs, 14931090276 residues  
 Word size : 0  
 Total number of hits satisfying chosen parameters: 138346  
 Minimum DB seq length: 0  
 Maximum DB seq length: 50  
 Post-processing: Listing first 45 summaries

Database : EST:\*  
 1: em\_estba:\*  
 2: em\_esthum:\*  
 3: em\_estin.\*  
 4: em\_estmu.\*  
 5: em\_estov.\*  
 6: em\_estpl.\*  
 7: em\_estro.\*  
 8: em\_htc.\*  
 9: gb\_est1.\*  
 10: gb\_est2.\*  
 11: gb\_htc.\*  
 12: gb\_est3.\*  
 13: gb\_est4.\*  
 14: gb\_est5.\*  
 15: em\_estfun.\*  
 16: em\_estom.\*  
 17: em\_gss\_hum.\*  
 18: em\_gss\_inv.\*  
 19: em\_gss\_pln.\*  
 20: em\_gss\_vrt.\*  
 21: em\_gss\_fun.\*  
 22: em\_gss\_mam.\*  
 23: em\_gss\_mus.\*  
 24: em\_gss\_pro.\*  
 25: em\_gss\_rod.\*  
 26: em\_gss\_phg.\*  
 27: em\_gss\_vrl.\*  
 28: gb\_gss1.\*  
 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
* Result No.	Score	Match Length	ID Description
1	43	2.0	50 9 AUI06827
2	41	2.0	50 9 AUI06825
3	40	1.9	50 9 AUI06826
4	35	1.7	50 9 AA564185

C	5	34	1.6	40	14	CF332441
C	6	33	1.6	33	13	BU431798
C	7	33	1.6	34	13	BU431799
C	8	33	1.6	39	14	CF327755
C	9	33	1.6	40	2	HSM001841
C	10	33	1.6	44	14	CF302212
C	11	33	1.6	44	14	CF305473
C	12	33	1.6	44	14	CF334384
C	13	33	1.6	45	10	BF582680
C	14	33	1.6	46	13	BX561724
C	15	33	1.6	46	14	CF332152
C	16	33	1.6	47	14	CF337040
C	17	33	1.6	48	14	CF333983
C	18	33	1.6	49	9	AA852759
C	19	33	1.6	49	9	A1316598
C	20	33	1.6	49	28	AZ587341
C	21	33	1.6	50	9	AA853120
C	22	33	1.6	50	9	AA617223
C	23	33	1.6	50	10	AW215755
C	24	33	1.6	50	12	BI496942
C	25	33	1.6	50	13	EX558006
C	26	33	1.6	50	13	EX699285
C	27	33	1.6	50	14	CA335626
C	28	32	1.5	32	10	AW327277
C	29	32	1.5	32	14	CF291773
C	30	32	1.5	32	14	CF299386
C	31	32	1.5	32	14	CF309233
C	32	32	1.5	32	14	CF309345
C	33	32	1.5	32	14	CF313717
C	34	32	1.5	32	14	CF321046
C	35	32	1.5	32	14	CF328471
C	36	32	1.5	32	14	CF331270
C	37	32	1.5	32	28	AZ459536
C	38	32	1.5	32	28	AZ470832
C	39	32	1.5	32	28	AZ611890
C	40	32	1.5	32	28	AZ778018
C	41	32	1.5	32	29	DB85L21T
C	42	32	1.5	33	9	AL587609
C	43	32	1.5	33	14	CF291613
C	44	32	1.5	33	14	CF311229
C	45	32	1.5	33	14	CF326967

ALIGNMENTS

RESULT 1  
 AUI06827  
 LOCUS  
 DEFINITION AUI06827 Sugano Homo sapiens cdna library Homo sapiens cDNA clone 50 bp mRNA linear EST 30-AUG-2001  
 HEP20988, mRNA sequence.  
 ACCESSION AUI06827.1 GI:13556348  
 VERSION AUI06827  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Seee, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source Location/Qualifiers
1..50 /organism="Homo sapiens"
/mol\_type="mRNA"
/db\_xref="taxon:9606"
/clone="HEP20988"
/clone\_lib="Sugano Homo sapiens cDNA library"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20 GCGGCGTACGGCGTTGGCCACCGTCTCTAGAAAAGAGTCTAG 62
8 GCGGCGTACGGCGTTGGCCACCGTCTCTAGAAAAGAGTCTAG 50

RESULT 2
AUI06825 Sugano Homo sapiens cDNA library EST 30-AUG-2001
LOCUS CAS01421, mRNA sequence.
DEFINITION AUI06825 Sugano Homo sapiens cDNA library EST 30-AUG-2001
ACCESSION CAS01421, mRNA sequence.
VERSION AUI06825.1 GI:113556346
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source Location/Qualifiers
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ORIGIN

Query Match 2.0%; Score 41; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
58 GTCAGCTCTGTTCCGAGAGCAGCGGCTGGCGTGGGCCAT 98
10 GTCAGCTCTGTTCCGAGAGCAGCGGCTGGCGTGGGCCAT 50

RESULT 3
AUI06826 Sugano Homo sapiens cDNA library EST 30-AUG-2001
LOCUS CAS01421, mRNA sequence.
DEFINITION AUI06826 Sugano Homo sapiens cDNA library EST 30-AUG-2001

CAS03470, mRNA sequence.
AUI06826 Sugano Homo sapiens cDNA library EST 04-SEP-1997
VERSION AUI06826.1 GI:13556347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
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/mol\_type="mRNA"
/db\_xref="taxon:9606"
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/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 1.9%; Score 40; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
43 GTCTCTAGAAAAGAGTCTGTTCCGAGAGCAGC 82
11 GTCTCTAGAAAAGAGTCTGTTCCGAGAGCAGC 50

RESULT 4
AA564185/c
LOCUS rj04d11.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone IMAGE:985365 3', mRNA sequence.
DEFINITION AA564185
ACCESSION AA564185.1 GI:2335824
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 203 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

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FEATURES
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        /clone="IMAGE:985365"
        /sex="male"
        /tissue_type="normal prostate"
        /lab_host="DH10B"
        /clone_lib="NCI_CGAP_Pr21"
        /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptor (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is not normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
  Query Match
  Best Local Similarity 1.7%; Score 35; DB 9; Length 50;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2064 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
Db 44 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 10
RESULT 5
CF332441/c
LOCUS
DEFINITION
  NACL--08-P05.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION
CF332441
VERSION
CF332441.1 GI:33813099
KEYWORDS
  Oryza sativa
SOURCE
  Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 40)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnaah@gbio.com, bhnaah@bio.myongji.ac.kr.
FEATURES
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        /lab_host="E.coli DH10B"
        /clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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QY 2063 TTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2096
Db 34 TTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11
RESULT 6
BU431798/c
LOCUS
DEFINITION
  60165590R1 NIH_MGC_66 Homo sapiens CDNA clone IMAGE:3855694 3',
  mRNA sequence.
ACCESSION
BU431798
VERSION
BU431798.1 GI:22770280
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
REFERENCE
  1 (bases 1 to 33)
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: DCID/DTP
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLCM570 row: c column: 23
  High quality sequence stop: 31.
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      /clone_lib="NIH_MGC_66"
      /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI;
  Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
  Average insert size 1.8 kb. Library constructed by Life
  Technologies."
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  Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 33 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11
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LOCUS
DEFINITION
  601655967R1 NIH_MGC_66 Homo sapiens CDNA clone IMAGE:3855737 3',
  mRNA sequence.
ACCESSION
BU431799
VERSION
BU431799.1 GI:22770281
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
REFERENCE
  1 (bases 1 to 34)
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  
```

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: DCTD/DFP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: InCyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 High quality sequence stop: 31.  
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 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.8 kb. Library constructed by Life  
 Technologies. "

ORIGIN  
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QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 34 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 8  
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 sativa cDNA clone NACL--02-F23, mRNA sequence.  
 ACCESSION CF327755  
 VERSION CF327755.1 GI:33803761  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1. (bases 1 to 39)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. .39

FEATURES source  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
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 /clone="NACL--02-F23"  
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 with oligoribonucleotides and then used as templates for

ORIGIN  
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 Best Local Similarity 100.0%; Pred. NO. 0;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 34 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

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 XX  
 AC AL037510;  
 XX  
 SV AL037510.1  
 XX  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
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 XX  
 KW EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN [1]  
 RP 1-40  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIFS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No sl sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX  
 FH Key Location/Qualifiers  
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 FT 1. .40  
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 FT Xl-2blue; sites NotI + SalI"  
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 4 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 10  
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 LOCUS  
 DEFINITION CF302212  
 44 bp mRNA linear EST 15-AUG-2003  
 7LEAF--07-114.b1 Rice leaf plasmid cDNA library II  
 (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--07-114, mRNA sequence.

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ORIGIN  
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 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 4 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36



ACCESSION CF302212  
 VERSION CF302212.1 GI:33673973  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 44)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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 RT-PCR."

FEATURES  
 source

ORIGIN

Query Match 1.6%; Score 33; DB 14; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 37 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 11  
 CF305473/c  
 LOCUS CF305473  
 DEFINITION Oryza sativa cDNA clone CLD1--01-M22, mRNA sequence.  
 ACCESSION CF305473  
 VERSION CF305473.1 GI:33677234  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 44)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /organism="Oryza sativa"

/mol\_type="mRNA"  
 /cultivar="Nackdong"  
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 /clone="CLD1--01-M22"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice cold treated leaf plasmid cDNA library  
 (CLD1)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was  
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 mRNA was reverse transcribed and then used for PCR."  
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 Query Match 1.6%; Score 33; DB 14; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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 QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 39 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 12  
 CF334384/c  
 LOCUS CF334384  
 DEFINITION JMT--03-K14.b1 ATJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa CDNA clone JMT--03-K14, mRNA sequence.  
 ACCESSION CF334384  
 VERSION CF334384.1 GI:33817097  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 44)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ATJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis Jasmonate Carboxyl  
 methyltransferase overexpression line."

FEATURES  
 source

ORIGIN

Query Match 1.6%; Score 33; DB 14; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 42 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 10

**RESULT 13**  
**BF582680**  
**LOCUS**  
**DEFINITION** BF582680 45 bp mRNA linear EST 12-DEC-2000  
 602094085F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4208373 5',  
 mRNA sequence.  
**ACCESSION** BF582680  
**VERSION** BF582680.1 GI:11656398  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
**REFERENCE** 1 (bases 1 to 45)  
**AUTHORS** Mammalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Mus.  
**TITLE** Mammalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Mus.  
**JOURNAL** NIH-MGC http://mgs.nci.nih.gov/.  
**COMMENT** National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strauberg, Ph.D.  
 Email: cgapsb-@mail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LHAM9772 row: j column: 22  
 High quality sequence stop: 45.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /clone="IMAGE:4208373"  
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 /clone\_lib="NCI\_CGAP\_Co24"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NotI;  
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 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

**FEATURES**  
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**ORIGIN**  
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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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**Db** 1 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33  
**RESULT 15**  
**CF332152**  
**LOCUS** CF332152 46 bp mRNA linear EST 18-AUG-2003  
**DEFINITION** NACL--08-I20.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--08-I20, mRNA sequence.  
**ACCESSION** CF332152  
**VERSION** CF332152.1 GI:33812528  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
 Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 46)  
**AUTHORS** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
**FEATURES**  
 source  
 Query Match 1.6%; Score 33; DB 10; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**QY** 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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**Db** 6 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 38  
**RESULT 14**  
**BX561724**  
**LOCUS** BX561724 46 bp mRNA linear EST 10-OCT-2003  
**DEFINITION** BX561724 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone t8e57d10\_g1c, mRNA sequence.  
**ACCESSION** BX561724  
**VERSION** BX561724.1 GI:33371526  
**KEYWORDS** EST.  
**SOURCE** Glossina morsitans morsitans  
**ORGANISM** Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscoidae; Glossinidae; Glossina.  
**REFERENCE** 1 (bases 1 to 46)  
**AUTHORS** Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
**TITLE** Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
**JOURNAL** Genome Biol. 4 (10), R63 (2003)

**FEATURES**  
 source  
 Query Match 1.6%; Score 33; DB 13; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**QY** 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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**Db** 1 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33  
**RESULT 15**  
**CF332152**  
**LOCUS** CF332152 46 bp mRNA linear EST 18-AUG-2003  
**DEFINITION** NACL--08-I20.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--08-I20, mRNA sequence.  
**ACCESSION** CF332152  
**VERSION** CF332152.1 GI:33812528  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
 Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 46)  
**AUTHORS** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
**FEATURES**  
 source  
 Query Match 1.6%; Score 33; DB 13; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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**Db** 1 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Query Match 1.6%; Score 33; DB 14; Length 46;  
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 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 5412 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 03:25:14 ; Search time 8116 Seconds  
(without alignments)  
11204.249 Million cell updates/sec

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Perfect score: 2098  
Sequence: 1 gggccattatggatgggg.....aaaaaaaaaaaaaaaaa 2098

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 9: gb\_pr.\*
- 10: gb\_ro.\*
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- 12: gb\_sy.\*
- 13: gb\_un.\*
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- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
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- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
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- 26: em\_ro.\*
- 27: em\_sts.\*
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- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
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- 32: em\_htg\_other.\*
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- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	34	1.6	45	6	AX287571	AX287571 Sequence
C 2	34	1.6	45	6	AX287575	AX287575 Sequence
C 3	34	1.6	46	6	AX287578	AX287578 Sequence
C 4	34	1.6	46	6	AX287582	AX287582 Sequence
C 5	33	1.6	46	6	AX287579	AX287579 Sequence
C 6	33	1.6	46	6	AX287583	AX287583 Sequence
C 7	33	1.6	49	6	E62856	E62856 Secretary p
C 8	32	1.5	33	6	BD011883	BD011883 Detection
C 9	32	1.5	37	6	I29931	I29931 Sequence 44
C 10	32	1.5	37	6	AX106972	AX106972 Sequence
C 11	32	1.5	38	6	E50766	E50766 Vector expr
C 12	32	1.5	40	6	A48799	A48799 Sequence 6
C 13	32	1.5	40	6	AR232955	AR232955 Sequence
C 14	32	1.5	43	6	AX225198	AX225198 Sequence
C 15	32	1.5	44	6	AX206861	AX206861 Sequence
C 16	32	1.5	45	6	E50989	E50989 Method for
C 17	32	1.5	50	6	I36502	I36502 Sequence 1
C 18	32	1.5	50	6	AR423115	AR423115 Sequence
C 19	32	1.5	50	6	AR423218	AR423218 Sequence
C 20	32	1.5	50	6	AX261361	AX261361 Sequence
C 21	32	1.5	50	6	BD118668	BD118668 EST and e
C 22	32	1.5	50	6	BD118771	BD118771 EST and e
C 23	32	1.5	50	6	BD170451	BD170451 Method of
C 24	31	1.5	41	6	AR309630	AR309630 Sequence
C 25	31	1.5	43	6	AX395321	AX395321 Sequence
C 26	31	1.5	43	6	AX443022	AX443022 Sequence
C 27	31	1.5	43	6	AX459616	AX459616 Sequence
C 28	31	1.5	44	6	AR038858	AR038858 Sequence
C 29	31	1.5	45	6	AR429142	AR429142 Sequence
C 30	31	1.5	45	6	AX838339	AX838339 Sequence
C 31	31	1.5	45	6	AX840840	AX840840 Sequence
C 32	31	1.5	45	6	BD016445	BD016445 Gene deri
C 33	31	1.5	50	6	BD132852	BD132852 Methods o
C 34	30	1.4	30	6	A43784	A43784 Sequence 9
C 35	30	1.4	30	6	A62991	A62991 Sequence 3
C 36	30	1.4	30	6	A62995	A62995 Sequence 7
C 37	30	1.4	30	6	AR179066	AR179066 Sequence
C 38	30	1.4	30	6	AR179070	AR179070 Sequence
C 39	30	1.4	30	6	E04638	E04638 Synthesized
C 40	30	1.4	30	6	I84450	I84450 Sequence 9
C 41	30	1.4	30	6	AX104902	AX104902 Sequence
C 42	30	1.4	30	6	AX104903	AX104903 Sequence
C 43	30	1.4	30	6	AX474673	AX474673 Sequence
C 44	30	1.4	30	6	AX474674	AX474674 Sequence
C 45	30	1.4	30	6	AX521609	AX521609 Sequence

ALIGNMENTS

RESULT 1  
 AX287571/c  
 LOCUS AX287571 Sequence 14 from Patent WO0177390. 45 bp DNA linear PAT 21-NOV-2001  
 DEFINITION AX287571  
 ACCESSION AX287571  
 VERSION AX287571.1 GI:17049337  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS abaraz A.P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 14 18-OCT-2001;  
 Molecular Staging, Inc. (US)

FEATURES Location/Qualifiers  
 source 1..45  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PI primer for use in allele discrimination"

Best Local Similarity 100.0%; Pred. No. 9e-07; DB 6; Length 45;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2065 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 34 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 4  
 AX287582/c  
 LOCUS AX287582 46 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 25 from Patent WO0177390.  
 ACCESSION AX287582  
 VERSION AX287582.1 GI:17049348  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS abarz A, P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 25 18-OCT-2001;  
 MOLECULAR Staging, Inc. (US)  
 FEATURES Location/Qualifiers  
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 /db\_xref="taxon:32630"  
 /note="PI primer for use in allele discrimination"

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QY 2065 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 37 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

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 LOCUS AX287575 45 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 18 from Patent WO0177390.  
 ACCESSION AX287575  
 VERSION AX287575.1 GI:17049341  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS abarz A, P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 18 18-OCT-2001;  
 MOLECULAR Staging, Inc. (US)  
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 Db 37 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 3  
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 LOCUS AX287578 46 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 21 from Patent WO0177390.  
 ACCESSION AX287578  
 VERSION AX287578.1 GI:17049344  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS abarz A, P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 21 18-OCT-2001;  
 MOLECULAR Staging, Inc. (US)  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PI primer for use in allele discrimination"

Query Match 1.6%; Score 34; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 9e-07; DB 6; Length 46;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2065 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
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 Db 34 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 5  
 AX287579/c  
 LOCUS AX287579 46 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 22 from Patent WO0177390.  
 ACCESSION AX287579  
 VERSION AX287579.1 GI:17049345  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS abarz A, P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 22 18-OCT-2001;  
 MOLECULAR Staging, Inc. (US)  
 FEATURES Location/Qualifiers  
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 /note="PI primer for use in allele discrimination"

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QY 2066 GAAAAA  
 |||  
 Db 38 GAAAAA

RESULT 6  
 AX287582/c  
 LOCUS AX287582 46 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 25 from Patent WO0177390.  
 ACCESSION AX287582  
 VERSION AX287582.1 GI:17049348  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS abarz A, P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 25 18-OCT-2001;  
 MOLECULAR Staging, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..46  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PI primer for use in allele discrimination"

Query Match 1.6%; Score 34; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 9e-07; DB 6; Length 46;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2065 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 34 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 5  
 AX287579/c  
 LOCUS AX287579 46 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 22 from Patent WO0177390.  
 ACCESSION AX287579  
 VERSION AX287579.1 GI:17049345  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS abarz A, P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 22 18-OCT-2001;  
 MOLECULAR Staging, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..46  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PI primer for use in allele discrimination"

Query Match 1.6%; Score 33; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06; DB 6; Length 46;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAA  
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 Db 38 GAAAAA

RESULT 6  
 AX287582/c  
 LOCUS AX287582 46 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 25 from Patent WO0177390.  
 ACCESSION AX287582  
 VERSION AX287582.1 GI:17049348  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS abarz A, P.  
 TITLE Process for allele discrimination utilizing primer extension  
 JOURNAL Patent: WO 0177390-A 25 18-OCT-2001;  
 MOLECULAR Staging, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..46  
 /organism="synthetic construct"  
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 /db\_xref="taxon:32630"  
 /note="PI primer for use in allele discrimination"



Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 12  
 A48799 A48799 40 bp DNA linear PAT 07-MAR-1997  
 LOCUS Sequence 6 from Patent WO9603528.  
 DEFINITION A48799  
 ACCESSION A48799  
 VERSION A48799.1 GI:2302466  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unclassified

REFERENCE 1 (bases 1 to 40)  
 AUTHORS Petrik,J., Allain,J. and Pearson,G.J.  
 TITLE OLIGONUCLEOTIDES AND THEIR USE  
 JOURNAL Patent: WO 9603528-A 6 08-FEB-1996;  
 LYNXVALE LTD (GB)  
 COMMENT Other publication AU 3118395 960222.  
 FEATURES Location/Qualifiers  
 source 1..40  
 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

ORIGIN  
 Query Match 1.5%; Score 32; DB 6; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 13  
 AR232955 AR232955 40 bp DNA linear PAT 20-DEC-2002  
 LOCUS Sequence 7 from patent US 6457426.  
 DEFINITION AR232955  
 ACCESSION AR232955  
 VERSION AR232955.1 GI:27275302  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 40)  
 AUTHORS Cruson,I.  
 TITLE Front tube furrow opener attachment  
 JOURNAL Patent: US 6457426-A 7 01-OCT-2002;  
 FEATURES Location/Qualifiers  
 source 1..40  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 1.5%; Score 32; DB 6; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 14  
 AX225198/c AX225198 43 bp DNA linear PAT 10-SEP-2001  
 LOCUS Sequence 7 from Patent WO0161033.  
 DEFINITION AX225198  
 ACCESSION AX225198

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 11  
 E50766 E50766 38 bp DNA linear PAT 31-JAN-2002  
 LOCUS Vector expressing full-length gene of RNA virus and utilization  
 DEFINITION thereof.  
 ACCESSION E50766  
 VERSION E50766.1 GI:18628191  
 KEYWORDS JP 2000152793-A/19.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 38)  
 AUTHORS Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.  
 TITLE Vector expressing full-length gene of RNA virus and utilization  
 JOURNAL Patent: JP 2000152793-A 19 06-JUN-2000;  
 TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI PHARMACEUT CO LTD

COMMENT OS Artificial Sequence  
 PN JP 2000152793-A/19  
 PD 06-JUN-2000  
 PE 24-JUN-1999 JP 1999178347  
 PF  
 PI MICHINORI OBARA,KYOKO OBARA,KAZUNARI TABIRA,JUNICHI MATSUZAKI,  
 PI HIROSHI OMORI  
 PC C12N15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC

FH Key Location/Qualifiers  
 FT source 1..38  
 FT /organism="synthetic construct"  
 FT /mol\_type="genomic DNA"  
 FT /db\_xref="taxon:32650"

FEATURES Location/Qualifiers  
 source 1..38  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32650"

ORIGIN  
 Query Match 1.5%; Score 32; DB 6; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;



VERSION AX225198.1 GI:15555219

KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Schouten,J.P.  
TITLE Multiplex ligatable probe amplification  
JOURNAL Patent: WO 0161033-A 7 23-AUG-2001;  
Schouten, Johannes Petrus (NL)

FEATURES Location/Qualifiers  
source 1..43

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic DNA"

ORIGIN

Query Match 1..5%; Score 32; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. NO. 1.1e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 12

RESULT 15

AX206861/c

LOCUS AX206861/c 44 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 7 from Patent WO0155391.

ACCESSION AX206861

VERSION AX206861.1 GI:15394685

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Jakobovits,A., Afar,D.E., Challita-Eid,P.M., Levin,E.,  
Mitchell,S.C. and Hubert,R.S.

TITLE 84p2a9: a prostate and testis specific protein highly expressed in

JOURNAL Prostate cancer

Patent: WO 0155391-A 7 02-AUG-2001;

Urogenesys, Inc. (US)

Location/Qualifiers

source 1..44

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

ORIGIN

Query Match 1..5%; Score 32; DB 6; Length 44;  
Best Local Similarity 100.0%; Pred. NO. 1.1e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098

Db 44 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 13

Search completed: July 2, 2004, 06:05:40  
Job time : 8130 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 03:23:53 ; Search time 822 Seconds
(without alignments)
10842.725 Million cell updates/sec

Title: US-09-445-223-2
Perfect score: 2098
Sequence: 1 ggcattatggtgatggg.....aaaaaaaaaaaaaaaaaaaaa 2098

Scoring table: OLIGO\_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3185356

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

- Database : N\_Geneseq\_29Jan04:\*
1: Geneseqn1980s:\*
2: Geneseqn1990s:\*
3: Geneseqn2000s:\*
4: Geneseqn2001as:\*
5: Geneseqn2001bs:\*
6: Geneseqn2002s:\*
7: Geneseqn2003as:\*
8: Geneseqn2003bs:\*
9: Geneseqn2003cs:\*
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Table with columns: Result No., Score, Query Match, Length, DB ID, Description. Contains 45 rows of search results.

Table with columns: C, 24, 32, 1.5, 43, 4, AAD17216, etc. Lists various identifiers and their associated values.

ALIGNMENTS

RESULT 1
ABZ04660
ID ABZ04660 standard; DNA; 50 BP.
XX ABZ04660;
DT 09-JAN-2003 (first entry)
DE Human leukocyte gene expression profiling probe SEQ ID NO 4651.
KW T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; ss.
OS Homo sapiens.
PN WC200257414-A2.
PD 25-JUL-2002.
PF 22-OCT-2001; 2001WO-US047856.
PR 20-OCT-2000; 2000US-0241994P.
PA 08-JUN-2001; 2001US-0296764P.
XX (BIOC-) BIOCARDIA INC.
Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J; Ly N, Woodward R, Quertermous T, Johnson F;
WPI; 2002-636525/68.
New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
Claim 1; Page 476; Opp; English.
The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient,







Query Match 1.6%; Score 33; DB 6; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 8  
 AAD27116  
 ID AAD27116 standard; RNA; 36 BP.  
 XX AC  
 XX XX

09-APR-2002 (first entry)  
 RNA template, AA used to direct RNA synthesis by HCV RNA polymerase.  
 Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;  
 lead compound; RNA polymerase; ss.  
 Unidentified.  
 US6322966-BI.  
 27-NOV-2001.  
 11-MAY-1999; 99US-00309670.  
 11-MAY-1999; 99US-00309670.  
 (ZHONG/) ZHONG W.  
 (HONG/) HONG Z.  
 (LAUJ/) LAU J Y N.

Zhong W, Hong Z, Lau JYN;  
 WPI; 2002-096587/13.  
 Assay system for hepatitis C virus replicase activity comprises RNA  
 template with unstable, small stemloop capable of forming copy-back  
 structure, viral non-structural protein 5B, nucleoside triphosphates,  
 buffer.  
 Example 1; Fig 1A; 10pp; English.

The present invention relates to an assay system for hepatitis C virus  
 (HCV) replicase activity. The assay system comprises an RNA template that  
 has an unstable, small stemloop at the 3' end capable of forming a copy-  
 back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,  
 and UTP nucleoside triphosphates (NTPs), where one of the NTP is  
 radiolabelled and an assay buffer that supports replication activity of  
 NS5B. The invention also relates to the identification of optimal  
 properties of an RNA template for copy-back self-priming RNA synthesis of  
 HCV. This activity can be used to screen for anti-HCV replicase compounds  
 or to characterise the biological relevance of lead compounds. The  
 optimal RNA templates can be used for developing a system to characterise  
 HCV NS5B polymerase mechanistically and kinetically and for designing  
 small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay  
 system of the invention is useful for detecting HCV polymerase. The assay  
 The nucleic acid synthesised by NS5B is detected by evaluating an  
 autoradiograph of reaction products separated by gel electrophoresis.  
 present sequence is RNA template, AA used to direct RNA synthesis by RNA  
 polymerase proteins of HCV, BVDV and poliovirus. This sequence is used in  
 the exemplification of the invention

Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 33; DB 6; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 9  
 AAD27117  
 ID AAD27117 standard; RNA; 36 BP.  
 XX AC  
 XX XX

09-APR-2002 (first entry)  
 RNA template, AU used to direct RNA synthesis by HCV RNA polymerase.  
 Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;  
 lead compound; RNA polymerase; ss.  
 Unidentified.  
 US6322966-BI.  
 27-NOV-2001.  
 11-MAY-1999; 99US-00309670.  
 11-MAY-1999; 99US-00309670.  
 (ZHONG/) ZHONG W.  
 (HONG/) HONG Z.  
 (LAUJ/) LAU J Y N.

Zhong W, Hong Z, Lau JYN;  
 WPI; 2002-096587/13.  
 Assay system for hepatitis C virus replicase activity comprises RNA  
 template with unstable, small stemloop capable of forming copy-back  
 structure, viral non-structural protein 5B, nucleoside triphosphates,  
 buffer.  
 Example 1; Fig 1A; 10pp; English.

The present invention relates to an assay system for hepatitis C virus  
 (HCV) replicase activity. The assay system comprises an RNA template that  
 has an unstable, small stemloop at the 3' end capable of forming a copy-  
 back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,  
 and UTP nucleoside triphosphates (NTPs), where one of the NTP is  
 radiolabelled and an assay buffer that supports replication activity of  
 NS5B. The invention also relates to the identification of optimal  
 properties of an RNA template for copy-back self-priming RNA synthesis of  
 HCV. This activity can be used to screen for anti-HCV replicase compounds  
 or to characterise the biological relevance of lead compounds. The  
 optimal RNA templates can be used for developing a system to characterise  
 HCV NS5B polymerase mechanistically and kinetically and for designing  
 small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay  
 system of the invention is useful for detecting HCV polymerase. The assay  
 The nucleic acid synthesised by NS5B is detected by evaluating an  
 autoradiograph of reaction products separated by gel electrophoresis.  
 present sequence is RNA template, AU used to direct RNA synthesis by RNA  
 polymerase proteins of HCV, BVDV and poliovirus. This sequence is used in  
 the exemplification of the invention

Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;  
 Query Match 1.6%; Score 33; DB 6; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 |||  
 Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

XX AC AAS95732;  
 XX DT 14-FEB-2002 (first entry)  
 XX DE Allele discrimination P1 primer #16.  
 XX KW Rolling circle amplification; single nucleotide polymorphism; anaemia;  
 KW exonuclease deficient DNA polymerase; amplification target circle; RCA;  
 KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;  
 KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;  
 KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;  
 KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;  
 KW melanoma; PCR primer; sequencing primer; probe.  
 XX OS Homo sapiens.  
 XX PN WO200177390-A2.  
 XX PD 18-OCT-2001.  
 XX PF 05-APR-2001; 2001WO-US011151.  
 XX PR 05-APR-2000; 2000US-0194843P.  
 XX PA (MOLE-) MOLECULAR STAGING INC.  
 XX PI Abarzua P;  
 XX DR WPI; 2002-049157/06.  
 XX PT Detecting single nucleotide polymorphism involves amplifying target  
 PT sequences using small primer probe that matches or mismatches to target  
 PT sequence and extending primer probe which is then detected.  
 XX PS Claim 15; Page 42; 67pp; English.  
 XX CC The invention relates to detecting single nucleotide polymorphisms by  
 CC contacting an allele-specific oligonucleotide primer (P1) with a target  
 CC polynucleotide to form a hybridisation complex, where the target sequence  
 CC is complementary to P1 at one end but the terminal nucleotide and the  
 CC third nucleotide from the terminal at the other end of P1 may not be  
 CC complementary. The complex is then contacted with an exonuclease  
 CC deficient DNA polymerase enzyme under conditions that promote extension  
 CC of P1 with the target DNA as the template, thereby forming an extended  
 CC segment of P1. Oligonucleotide probes hybridising to one or more target  
 CC polynucleotides distinguish between matched and mismatched 3' ends, hence  
 CC the absence of sequence amplification indicates the presence of a single  
 CC nucleotide mismatch. Primer sequences complementary to a sequence on an  
 CC amplification target circle can be used in rolling circle amplification  
 CC (RCA). The method is useful for diagnosing a disease caused by, induced  
 CC by or related to a mutation in at least one gene, such as Parkinson's  
 CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington  
 CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,  
 CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,  
 CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and  
 CC melanoma. Sequences AAS95711-AAS95745 represent primers, targets and  
 CC fluorescence decorators used in the detection of RCA products  
 XX SQ Sequence 46 BP; 2 A; 3 C; 0 G; 41 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 33; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 DB 38 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6  
 RESULT 12  
 AAS95736/c  
 ID AAS95736 standard; DNA; 46 BP.

RESULT 10  
 AAD27125  
 ID AAD27125 standard; RNA; 37 BP.  
 XX AC AAD27125;  
 XX DT 09-APR-2002 (first entry)  
 XX DE RNA template, (AU)2 used to direct RNA synthesis by HCV RNA polymerase.  
 XX KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;  
 KW lead compound; RNA polymerase; ss.  
 XX OS Unidentified.  
 XX PN US6322966-B1.  
 XX PD 27-NOV-2001.  
 XX PF 11-MAY-1999; 99US-00309670.  
 XX PR 11-MAY-1999; 99US-00309670.  
 XX PA (ZHON/) ZHONG W.  
 PA (HONG/) HONG Z.  
 PA (LAUJ/) LAU J Y N.  
 PI Zhong W, Hong Z, Lau JYN;  
 XX DR WPI; 2002-096587/13.  
 XX PT Assay system for hepatitis C virus replicase activity comprises RNA  
 PT template with unstable, small stemloop capable of forming copy-back  
 PT structure, viral non-structural protein 5B, nucleoside triphosphates,  
 PT buffer.  
 XX PS Example 1; Fig 2A; 10pp; English.  
 XX CC The present invention relates to an assay system for hepatitis C virus  
 CC (HCV) replicase activity. The assay system comprises an RNA template that  
 CC has an unstable, small stemloop at the 3' end capable of forming a copy-  
 CC back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,  
 CC and UTP nucleoside triphosphates (NTPs), where one of the NTP is  
 CC radiolabelled and an assay buffer that supports replication activity of  
 CC NS5B. The invention also relates to the identification of optimal  
 CC properties of an RNA template for copy-back self-priming RNA synthesis of  
 CC HCV. This activity can be used to screen for anti-HCV replicase compounds  
 CC or to characterise the biological relevance of lead compounds. The  
 CC optimal RNA templates can be used for developing a system to characterise  
 CC HCV NS5B polymerase mechanistically and kinetically and for designing  
 CC small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay  
 CC system of the invention is useful for detecting HCV replicase activity.  
 CC The nucleic acid synthesised by NS5B is detected by evaluating an  
 CC autoradiograph of reaction products separated by gel electrophoresis. The  
 CC present sequence is RNA template, (AU)2 used to direct RNA synthesis by  
 CC RNA polymerase proteins of HCV, BVDV and poliovirus. This sequence is used  
 CC in the exemplification of the invention  
 XX SQ Sequence 37 BP; 33 A; 0 C; 2 G; 0 T; 2 U; 0 Other;  
 Query Match 1.6%; Score 33; DB 6; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 DB 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34  
 RESULT 11  
 AAS95732/c  
 ID AAS95732 standard; DNA; 46 BP.



.XX AAS95736;  
 AC 14-FEB-2002 (first entry)  
 XX Allele discrimination P1 primer #20.  
 DT Rolling circle amplification; single nucleotide polymorphism: anaemia;  
 DE exonuclease deficient DNA polymerase; amplification target circle; RCA;  
 DE Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;  
 DE Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;  
 DE diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;  
 DE lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;  
 DE melanoma; PCR primer; sequencing primer; probe.  
 OS Homo sapiens.  
 XX W0200177390-A2.  
 XX 18-OCT-2001.  
 PD 05-APR-2001; 2001WO-US011151.  
 XX 05-APR-2000; 2000US-0194843P.  
 PR (MOLE-) MOLECULAR STAGING INC.  
 XX Abarzua P;  
 PI WPI; 2002-049157/06.  
 DR Detecting single nucleotide polymorphism involves amplifying target  
 PT sequences using small primer probe that matches or mismatches to target  
 PT sequence and extending primer probe which is then detected.  
 XX Claim 15; Page 43; 67pp; English.  
 CC The invention relates to detecting single nucleotide polymorphisms by  
 CC contacting an allele-specific oligonucleotide primer (P1) with a target  
 CC polynucleotide to form a hybridisation complex, where the target sequence  
 CC is complementary to P1 at one end but the terminal nucleotide and the  
 CC third nucleotide from the terminal at the other end of P1 may not be  
 CC complementary. The complex is then contacted with an exonuclease  
 CC deficient DNA polymerase enzyme under conditions that promote extension  
 CC of P1 with the target DNA as the template, thereby forming an extended  
 CC polynucleotide. The absence of sequence mismatch between hybridising to one or more target  
 CC nucleotide mismatch. Primer sequences complementary to a sequence on an  
 CC (RCA). The method is useful for diagnosing a disease caused by, induced  
 CC by or related to a mutation in at least one gene, such as Parkinson's  
 CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington  
 CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,  
 CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and  
 CC melanoma. Sequences AAS95711-AAS95745 represent primers, targets and  
 CC fluorescence decorators used in the detection of RCA products  
 XX  
 SQ Query Sequence 46 BP; 1 A; 3 C; 0 G; 42 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 33; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 DB 38 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

XX AAV02146;  
 AC 12-MAY-1998 (first entry)  
 XX Human secreted protein AKS33 3' portion including the polyA tail.  
 DE Human; secreted protein; ATCC 98026; cytokine; immunomodulation;  
 DE cell proliferation; differentiation; regulation; ds.  
 DE Homo sapiens.  
 XX W0973739123-A2.  
 XX 23-OCT-1997.  
 PD 14-APR-1997; 97WO-US006139.  
 XX 18-APR-1996; 96US-00634325.  
 PR (GEM) GENETICS INST INC.  
 XX Jacobs K, McCoy JM, Racie LA, Lavallie ER, Merberg D;  
 PI Spaulding V;  
 XX WPI; 1997-526460/48.  
 DR New secreted proteins encoded clones present in ATCC 98026 - possibly  
 XX having cytokine, cell proliferation/differentiation regulating,  
 XX immunomodulating and many other activities.  
 PS Disclosure; Page 86; 139pp; English.  
 CC The present sequence encodes a portion of a novel human secreted protein  
 CC deposited under accession number ATCC 98026. The secreted protein can be  
 CC used to determine biological activity, to raise antibodies, as tissue  
 CC markers, to isolate cognate ligands or receptors, to identify agents that  
 CC modulate their interactions and as nutritional supplements. It may also  
 CC have a very wide range of biological activities although no evidence for  
 CC any is provided in the specification. Typical of these are cytokine, cell  
 CC proliferation/differentiation modulating activity or induction of other  
 CC cytokines; immunostimulating/immunosuppressant activities (e.g. for  
 CC treating human immunodeficiency virus infection, cancer, autoimmune  
 CC diseases and allergy); regulation of haematopoiesis (e.g. for treating  
 CC anaemia or as adjunct to chemotherapy); stimulation of growth of bone,  
 CC cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds,  
 CC periodontal disease, neurological diseases stroke, fibrosis); inhibition  
 CC or stimulation of follicle stimulating hormone (for control of fertility)  
 CC ; chemocactic and chemokinetic activities (e.g. for treating infections,  
 CC tumours); haemostatic or thrombolytic activity (e.g. for treating  
 CC haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g.  
 CC for treating septic shock, Crohn's disease); as antimicrobials; for  
 CC treating psoriasis or other hyperproliferative disease; for regulation of  
 CC metabolism, behaviour, and many others. Also contemplated is the use of  
 CC the corresponding nucleic acid in gene therapy procedures  
 XX  
 SQ Query Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 33; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 DB 4 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 14  
 AAV02146  
 ID AAT88080 standard; cDNA; 49 BP.  
 XX  
 AC AAT88080;  
 XX

DT 14-MAY-1998 (first entry)  
 XX 3' portion of cDNA clone encoding secreted protein AK533.  
 DE Human, secreted protein; research; treatment; AM533; 3' portion; ds.  
 XX Homo sapiens.  
 XX WO9739122-A2.  
 XX 23-OCT-1997.  
 XX 11-APR-1997; 97WO-US006042.  
 XX 12-APR-1996; 96US-00631184.  
 XX (MURO-) MURO PHARM INC.  
 XX Theoharides TC;  
 XX WPI; 1997-526459/48.  
 XX Human and murine secreted proteins - useful in research or treatment of  
 PT diseases or disorders related to their function.  
 XX Disclosure; Page 86; 140pp; English.  
 XX The present sequence is the 3' portion of a cDNA clone encoding a human  
 CC secreted protein, which may have nutritional uses, or cytokine and cell  
 CC proliferation/differentiation, immune stimulating or suppressing,  
 CC haematopoiesis regulating, tissue growth, activin/inhibin,  
 CC chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand,  
 CC anti-inflammatory or tumour inhibitor activities. It can also be used to  
 CC research or treat diseases/disorders related to its function. The partial  
 CC cDNA clone AP162 was 1st isolated from a human adult placenta cDNA  
 CC library. The partial cDNA clones AM931, AM610, AM340, AM282, AK647,  
 CC AK583, AK533 and AK296 were 1st isolated from a human foetal kidney cDNA  
 CC library. The partial cDNA clones H617 and B89 were 1st isolated from a  
 CC human peripheral blood monocyte cell (Th1 or Th2) cDNA library. The  
 CC partial cDNA clone AW191 was 1st isolated from a human ovary (PA-1  
 CC teratocarcinoma) cDNA library. The partial cDNA clones AT211, AT205 and  
 CC AT319 were 1st isolated from a human lymphocyte and dendritic cell cDNA  
 CC library. The partial cDNA clones AS34 and AS32 were 1st isolated from a  
 CC human foetal brain cDNA library. The partial cDNA clone AE260 was 1st  
 CC isolated from a human adult retina cDNA library. The partial cDNA clones  
 CC K640 and K39 were 1st isolated from a murine bone marrow (stromal cell  
 CC line FCM-4) cDNA library  
 XX SQ Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 33; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 4 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 15  
 .AAN70278/C  
 ID AAN70278 standard; DNA; 32 BP.  
 XX \*AC AAN70278;  
 XX 03-OCT-2002 (revised)  
 DT 26-MAY-1991 (first entry)  
 XX Sequence of scissile link probe MRC068 (HL).  
 XX Hybridisation; probe; ss.  
 XX Synthetic.

XX EP227976-A.  
 XX 08-JUL-1987.  
 XX 04-DEC-1986; 86EP-00116906.  
 XX 05-DEC-1985; 85US-00805279.  
 XX (MEIO-) MEIOGENICS INC.  
 XX Duck P, Bender R, Crosby W, Robertson JG;  
 XX WPI; 1987-186567/27.  
 XX Synthetic nucleic acid probes - comprising two nucleic acid sequences  
 PT linked by a scissile linkage.  
 XX Example; p29; 46pp; English.  
 XX The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and  
 CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile  
 CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA  
 CC or RNA sequences in a test soln. The scissile link probes may be PL  
 CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid  
 CC Support). The differential liability of DNA and RNA may be exploited in a  
 CC heterogeneous system when the scissile linkage is an RNA molecule. In the  
 CC examples, counter probe molecules 9 through 16 were used to determine  
 CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing  
 CC OS field.)  
 XX SQ Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;  
 Query Match 1.5%; Score 32; DB 1; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 0.027;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

Search completed: July 2, 2004, 03:50:02  
 Job time : 824 secs